Amendments to the Claims

Please cancel Claims 5-26, 41, 44-46 and 48. Please amend Claim 4. Please add new Claims 49 and 50. The Claim Listing below will replace all prior versions of the claims in the application:

Claim Listing

1. (Withdrawn) An isolated nucleic acid molecule encoding a protein with a RING-finger domain and 6 NHL-motifs wherein the protein is associated with Lafora's disease.

2. (Withdrawn) A nucleic acid according to Claim 1 having a sequence comprising SEQ ID NO:1 or SEQ ID NO:3.

3. (Withdrawn) An isolated nucleic acid molecule according to Claim 1 comprising
   (a) a nucleic acid sequence comprising SEQ ID NO:1 or SEQ ID NO:3, wherein T can also be U;
   (b) a nucleic acid sequence complementary to (a);
   (c) a nucleic acid sequence that has substantial sequence homology to a nucleic acid sequence of (a) or (b);
   (d) a nucleic acid sequence that is an analog of a nucleic acid sequence of (a), (b) or (c); or
   (e) a nucleic acid sequence that hybridizes to a nucleic acid sequence of (a), (b), (c) or (d) under stringent hybridization conditions.

4. (Currently amended) A method of detecting the presence of, or predisposition to, Lafora's disease in a human, wherein the Lafora's disease is associated with a mutation in the EPM2B gene, comprising detecting ~~a missense, nonsense, insertion, deletion, point mutation or frameshift mutation in the EPM2B gene contained in a nucleic acid sequence in a sample obtained from the human, wherein the EPM2B gene comprises SEQ ID NO:~~

~~1, and wherein the mutation affects a portion of the EPM2B gene encoding a RING finger domain or an NHL motif of SEQ ID NO. 1 and wherein detection of a mutation indicates the presence of, or predisposition to, Lafora's disease in the human~~ a C to G change at nucleotide number 205 in the EPM2B gene sequence comprising SEQ ID NO:1.

5-33. (Canceled)

34. (Withdrawn) An isolated protein containing a RING-finger domain and six NHL domains which protein is associated with Lafora's disease.

35. (Withdrawn) A protein according to Claim 34 having the amino acid sequence comprising SEQ ID NO:2 or SEQ ID NO:4.

36. (Withdrawn) A method for detecting Lafora's disease comprising detecting a mutation in a protein according to Claim 34.

37. (Withdrawn) A method according to Claim 36 comprising detecting a mutation in the EPM2B protein as indicated in Table 1.

38. (Withdrawn) A kit for carrying out the method of Claim 4 comprising reagents for the detection of a mutation in a nucleic acid sequence comprising SEQ ID NO:1 or SEQ ID NO:3.

39. (Withdrawn) A kit for carrying out the method of Claim 36 comprising reagents for the detection of a mutation in a protein sequence comprising SEQ ID NO:2 or SEQ ID NO:5.

40-41. (Canceled)

42. (Withdrawn) A method for detecting the presence or absence of Lafora's disease comprising detecting a mutation in a protein according to claim 35.

43. (Previously presented) A method of detecting the presence or absence of a mutation in a nucleic acid in a test sample obtained from a human, wherein the test sample contains the EPM2B gene, the method comprising the steps of:

(a) analyzing the test sample containing the EPM2B gene to determine the nucleic acid sequence of the gene;

(b) comparing the nucleic acid sequence of the gene in the test sample to the nucleic acid sequence set forth in SEQ ID NO:1; and

(c) determining the differences, if any, between the sequence of the EPM2B gene in the test sample and the nucleic acid sequence set forth in SEQ ID NO:1, thereby detecting the presence or absence of a mutation in the EPM2B gene of the test sample.

44-46 (Canceled)

47. (Previously Presented) A method of detecting the presence of an EPM2B gene in a human comprising analyzing a nucleic acid test sample obtained from the human for the presence of said EPM2B gene, wherein said EPM2B gene comprises SEQ ID NO: 1.

48. (Canceled)

49. (New) The method of Claim 4 further comprising detecting one or more mutations in said EPM2B gene selected from the group consisting of:

(a) a T to A change at nucleotide number 76 in the EPM2B gene sequence comprising SEQ ID NO:1;

(b) a deletion of nucleotides GA at nucleotide positions 1048 and 1049 in the EPM2B gene sequence comprising SEQ ID NO:1;

(c) a deletion of nucleotides AG at nucleotide positions 468 and 469 in the EPM2B gene sequence comprising SEQ ID NO:1;

(d) a deletion of nucleotide G at nucleotide number 992 in the EPM2B gene sequence comprising SEQ ID NO:1;

(e) a deletion of 10 bp at nucleotide positions 373 to 382 in the EPM2B gene sequence comprising SEQ ID NO:1;

(f) a deletion of 32 bp at nucleotide positions 661 to 692 in the EPM2B gene sequence comprising SEQ ID NO:1;

(g) a T to C change at nucleotide number 260 in the EPM2B gene sequence comprising SEQ ID NO:1;

(h) a A to C change at nucleotide number 905 in the EPM2B gene sequence comprising SEQ ID NO:1;

(i) a T to C change at nucleotide number 98 in the EPM2B gene sequence comprising SEQ ID NO:1;

(j) an insertion of 2 Ts at nucleotide number 892 in the EPM2B gene sequence comprising SEQ ID NO:1;

(k) a G to A change at nucleotide number 436 in the EPM2B gene sequence comprising SEQ ID NO:1;

(l) a deletion of nucleotide T at nucleotide number 1100 in the EPM2B gene sequence comprising SEQ ID NO:1;

(m) a deletion of nucleotide T at nucleotide position 606 in the EPM2B gene sequence comprising SEQ ID NO:1;

(n) a A to T change at nucleotide number 923 in the EPM2B gene sequence comprising SEQ ID NO:1;

(o) a G to T change at nucleotide number 580 in the EPM2B gene sequence comprising SEQ ID NO:1;

(p) a G to T change at nucleotide number 199 in the EPM2B gene sequence comprising SEQ ID NO:1;

(q) a G to A change at nucleotide number 838 in the EPM2B gene sequence comprising SEQ ID NO:1;

(r) a C to T change at nucleotide number 676 in the EPM2B gene sequence comprising SEQ ID NO:1;

(s) a deletion of nucleotide A at nucleotide position 468 in the EPM2B gene sequence comprising SEQ ID NO:1; and

(t) a deletion of nucleotide C at nucleotide position 204 in the EPM2B gene sequence comprising SEQ ID NO:1.

50. (New) The method of Claim 43 wherein the test sample is amplified using suitable PCR primer sequences prior to analysis.